In the Application:

Please delete the sequence listing as filed and insert the amended sequence listing enclosed herewith.

In the Specification:

At page 1, after the heading CROSS REFERENCE TO RELATED APPLICATIONS please amend the paragraph beginning at line 5 as follows:

The present application: 1) is a continuation-in-part of U.S. application Serial No. 10/323,233 filed December 18, 2002, now abandoned; 2) is a continuation-in-part of U.S. application Serial No. 10/326,051 filed December 18, 2002, now abandoned; 3) is a continuation-in-part of U.S. application Serial No. 10/325,526 filed December 18, 2002, now abandoned; 4) is a continuation-in-part of U.S. application Serial No. 10/325,527 filed December 18, 2002, now abandoned; 5) is a continuation-in-part of U.S. application Serial No. 09/798,007 filed March 2, 2001, now abandoned; 6) claims the benefit of U.S. provisional application Serial No. 60/431,319 filed December 6, 2002; 7) claims the benefit of U.S. provisional application Serial No. 60/443,443 filed January 29, 2003; 8) claims the benefit of U.S. provisional application Serial No. 60/443,788 filed January 30, 2003; 9) claims the benefit of U.S. provisional application Serial No. 60/447,529 filed February 14, 2003; each of which is incorporated herein by reference in its entirety.

At page 1, after the heading STATEMENT OF GOVERNMENT SUPPORT please amend the paragraph beginning at line 16 as follows:

This invention was made with United States Government support under DARPA/SPO contract ~~4400044016~~ MDA972-00-C-0053. The United States Government has certain rights in the invention.

At page 10, please amend the paragraph beginning at line 12 as follows:

Figure 3 is a schematic diagram showing conserved regions in RNase P. Bases in

capital letters are greater than 90% conserved; bases in lower case letters are 80-90% conserved; filled circles designate bases which are 70-80% conserved; and open circles designate bases that are less than 70% conserved. The nucleotide sequence fo RNase P is SEQ ID NO: 378.

At page 10, please amend the paragraph beginning at line 16 as follows:

Figure 4 is a schematic diagram of base composition signature determination using nucleotide analog "tags" to determine base composition signatures. The "Watson" strand is SEQ ID NO: 349 and the "Crick" strand is SEQ ID NO: 380.

At page 11, please amend the paragraph beginning at line 7 as follows:

Figure 13 is a portion of a secondary structure defining database according to one embodiment of the present invention, where two examples of selected sequences are displayed graphically thereunder, SEQ ID NO: 381 and SEQ ID NO: 382.